

GenCore version 5.1.6  
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OM protein - protein search, using sw model  
Run on: March 3, 2005, 17:05:58 ; Search time 176 Seconds  
(without alignments)  
75.648 Million cell updates/sec

Title: US-09-733-239-1  
Perfect score: 139  
Sequence: 1 RILAVERYLKDQQLLGIGGSGKLLIC 26

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03:  
1: uniprot\_sprot:  
2: uniprot\_trembl:  
\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query	Score	Match Length	DB ID	Description
1	139	100.0	117	2 Q9YRU1	Q9yru1 human immun
2	139	100.0	117	2 Q9YYZ9	Q9yyz9 human immun
3	139	100.0	118	2 Q6WH32	Q6wh32 human immun
4	139	100.0	122	2 Q6DL09	Q6dl09 human immun
5	139	100.0	122	2 Q6DL62	Q6dl62 human immun
6	139	100.0	122	2 Q6WH41	Q6wh41 human immun
7	139	100.0	122	2 Q7ZJR4	Q7zjr4 human immun
8	139	100.0	122	2 Q9EA97	Q9ea97 human immun
9	139	100.0	122	2 Q9QIU3	Q9qiuj3 human immun
10	139	100.0	122	2 Q9WQZ3	Q9wqz3 human immun
11	139	100.0	122	2 Q9YXP4	Q9yxp4 human immun
12	139	100.0	123	2 Q8AEX2	Q8aex2 human immun
13	139	100.0	134	2 Q69BW3	Q69bw3 human immun
14	139	100.0	144	2 Q7ZCD6	Q7zcd6 human immun
15	139	100.0	144	2 Q7ZCD7	Q7zcd7 human immun
16	139	100.0	145	2 Q7ZC48	Q7zc48 human immun
17	139	100.0	145	2 Q7ZC52	Q7zc52 human immun
18	139	100.0	147	2 Q6JFL9	Q6jfl9 human immun
19	139	100.0	155	2 Q8J3N1	Q8j3n1 human immun
20	139	100.0	357	2 Q78119	Q78119 human immun
21	139	100.0	358	2 Q78120	Q78120 human immun
22	139	100.0	588	2 Q993A7	Q993a7 human immun
23	139	100.0	588	2 Q993A8	Q993a8 human immun
24	139	100.0	589	2 Q993B1	Q993b1 human immun
25	139	100.0	590	2 Q993A9	Q993a9 human immun
26	139	100.0	616	2 Q993B0	Q993b0 human immun
27	139	100.0	618	2 Q993B2	Q993b2 human immun
28	139	100.0	727	2 Q9Q723	Q9q723 human immun
29	139	100.0	746	2 Q6QLJ1	Q6qlj1 human immun
30	139	100.0	746	2 Q6QLJ3	Q6qlj3 human immun
31	139	100.0	747	2 Q70607	Q70607 human immun

RESULT 1					
ID	Q9YRU1	PRELIMINARY;	PRT;	117 AA.	
AC	Q9YRU1;				
DT	01-MAY-1999	(TrEMBLrel. 10, Created)			
DT	01-MAY-1999	(TrEMBLrel. 10, Last sequence update)			
DT	01-JUN-2003	(TrEMBLrel. 24, Last annotation update)			
DE	Envelope glycoprotein (Fragment).				
GN	Name=env;				
OS	Human immunodeficiency virus 1.				
OC	Viruses; Retroviridae; Lentivirus.				
NCBI_TaxID	11676;				
RN	[1]				
SEQUENCE FROM N.A.					
RP	SEQUENCE FROM N.A.				
RC	STRAIN=96USCM48;				
RA	Ellenberger D.L., Pau C.-P., Paul S., Kalish M.,				
RA	Sullivan P.J., Do A., Storck C., Schable C.A., Wise H., Tetteh C.,				
RA	Jones J., Ward J.;				
RL	Submitted (OCT-1998) to the EMBL/GenBank/DDJB databases.				
DR	EMBL; AF096324; AAD04399.1; -.				
DR	HSSP; Q88007; 1QBZ.				
DR	SEQUENCE FROM N.A.				
DR	GO; GO:0016021; C:integral membrane; IEA.				
DR	GO; GO:0019028; C:viral capsid; IEA.				
DR	GO; GO:0019031; C:viral envelope; IEA.				
DR	GO; GO:0005198; P:structural molecule activity; IEA.				
DR	InterPro; IPR000328; Env GP41.				
DR	Pfam; PF00517; GP41; 1.				
KW	Coat protein; Envelope protein; Glycoprotein; Transmembrane.				
FT	NON-TER	1			
FT	NON-TER	117			
SQ	SEQUENCE	117 AA;	13986 MW;	4719FD6EB98E42E3	CRC64;
Query Match	100.0%	Score 139;	DB 2;	Length 117;	
Best Local Similarity	100.0%	Pred. No. 1.	1.8e-13;		
Matches 26;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
OY	1 RILAVERYLKDQQLLGIGGSGKLLIC 26				
Db	19 RILAVERYLKDQQLLGIGGSGKLLIC 44				
RESULT 2					
ID	Q9YYZ9	PRELIMINARY;	PRT;	117 AA.	
AC	Q9YYZ9;				
DT	01-MAY-1999	(TrEMBLrel. 10, Created)			
DT	01-MAY-1999	(TrEMBLrel. 10, Last sequence update)			
DT	01-JUN-2003	(TrEMBLrel. 24, Last annotation update)			
DE	GP41 (Fragment).				
GN	Name=env;				
OS	Human immunodeficiency virus 1.				
OC	Viruses; Retroviridae; Lentivirus.				
NCBI_TaxID	11676;				
RN	[1]				

RP SEQUENCE FROM N.A.  
 RC STRAIN=171.005;  
 RA Brennan C.A., Lund J.K., Golden A., Yamaguchi J., Vallari A.S.,  
 RA Phillips J.F., Kataaha P.K., Jackson J.B., Devare S.G.;  
 RA Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.  
 RL EMBL; AF006876; ADD01320.1; -.  
 DR HSSP; Q91JQ8; 1GZL.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0019028; C:viral capsid; IEA.  
 DR GO; GO:0019031; C:viral envelope; IEA.  
 DR GO; GO:0005198; F:structural molecule activity; IEA.  
 DR InterPro; IPR000328; Env\_GP41.  
 DR Pfam; PF00517; GP41; 1.  
 KW Coat protein; Glycoprotein; Transmembrane.  
 FT NON-TER 1 1  
 PT NON-TER 117 117  
 SQ SEQUENCE 117 AA; 13970 MW; 4B0F82FC9AF0756D CRC64;

Query Match Score 139; DB 2; Length 117;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-13;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLLGIGWGCGSKLIC 26  
 23 RILAVERYLKDQQLLGIGWGCGSKLIC 48

RESULT 3  
 ID Q6WH32 PRELIMINARY; PRT; 118 AA.  
 AC Q6WH32;  
 DT 05-JUL-2004 (TREMBLrel. 27, Created)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
 DE Envelope glycoprotein (Fragment).  
 GN Name=env;  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=14715797;  
 RA Pires I.L., Soares M.A., Speranza F.A.B., Ishii S.K., Vieira M.C.G.,  
 RA Gouveia M.I.F.S., Guimaraes M.A.A.M., De Oliveira F.E.,  
 RA Magnanini M.M.F., Brindeiro R.M., Tanuri A.;  
 RT "Prevalence of human immunodeficiency virus drug resistance mutations  
 and subtypes in drug-naïve, infected individuals in the army health  
 service of Rio de Janeiro, Brazil.";  
 RT J. Clin. Microbiol. 42:426-430(2004).  
 RL EMBL; AY285064; AAQ68127.1; -.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0019028; C:viral capsid; IEA.  
 DR GO; GO:0019031; C:viral envelope; IEA.  
 DR GO; GO:0005198; F:structural molecule activity; IEA.  
 DR InterPro; IPR000328; Env\_GP41.  
 DR Pfam; PF00517; GP41; 1.  
 KW Coat protein; Envelope protein; Glycoprotein; Transmembrane.  
 FT NON-TER 1 1  
 SQ SEQUENCE 118 AA; 14303 MW; FC6437BD5749A4B8 CRC64;

Query Match Score 139; DB 2; Length 118;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-13;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLLGIGWGCGSKLIC 26  
 15 RILAVERYLKDQQLLGIGWGCGSKLIC 40

RESULT 4  
 ID Q6DL09 PRELIMINARY; PRT; 122 AA.

AC Q6DL09;  
 DT 25-OCT-2004 (TREMBLrel. 28, Created)  
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN Name=env;  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kalish M.L., Robbins K.E., Pieniazek D., Schaefer A., Nzilambi N.,  
 RA Quinn T.C., StLouis M.E., Youngpairoj A.S., Phillips J., Jaffe H.W.,  
 RA Folks T.M.;  
 RA "Recombinant viruses and early global HIV-1 epidemic.";  
 RL Emerg. Infect. Dis. 10:1227-1234 (2004).  
 DR GO; GO:0019031; C:viral envelope; IEA.  
 DR GO; GO:0005198; F:structural molecule activity; IEA.  
 DR InterPro; IPR000328; Env\_GP41.  
 DR Pfam; PF00517; GP41; 1.  
 KW Coat protein; Envelope protein; Glycoprotein; Transmembrane.  
 FT NON-TER 1 1  
 FT NON-TER 122 122  
 SQ SEQUENCE 122 AA; 14712 MW; 9D69569A666BD069 CRC64;

Query Match Score 139; DB 2; Length 122;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-13;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLLGIGWGCGSKLIC 26  
 19 RILAVERYLKDQQLLGIGWGCGSKLIC 44

Db

RESULT 6		FT NON-TER 122 122	SQ SEQUENCE 122 AA; 14777 MW; AE2C9F40DF21CCFB CRC64;
Q6WH41	PRELIMINARY;	PRT; 122 AA.	
ID Q6WH41;			
AC Q6WH41;			
DT 05-JUL-2004 (TREMBLrel. 27, Created)			
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)			
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)			
DE Envelope glycoprotein (Fragment).			
GN Name=env;			
OS Human immunodeficiency virus 1.			
OC Viruses; Retroviridae; Lentivirus.			
OX NCBI_TaxID=11676;			
RN [1]			
RP SEQUENCE FROM N.A.			
RX PubMed=14715797;			
RA Pires I.L., Soares M.A., Speranza F.A.B., Ishii S.K., Vieira M.C.G., Gouveia M.I.F.S., Guimaraes M.A.A.M., De Oliveira F.E., Magnanini M.M.F., Brindeiro R.M., Tanuri A.;			
RA "Prevalence of human immunodeficiency virus drug resistance mutations and subtypes in drug-naïve, infected individuals in the army health service of Rio de Janeiro, Brazil." J. Clin. Microbiol. 42:426-430(2004).			
RL EMBL; AY285055; AAQ68118.1; -.			
DR GO; GO:0016021; C:integral to membrane; IEA.			
DR GO; GO:0019028; C:viral capsid; IEA.			
DR GO; GO:0019031; C:viral envelope; IEA.			
DR GO; GO:0005198; F:structural molecule activity; IEA.			
DR InterPro; IPR000328; Env_GP41.			
DR PFam; PF00517; GP41; 1.			
KW Coat protein; Envelope protein; Glycoprotein; Transmembrane.			
FT NON-TER 1 1			
FT NON-TER 122 AA; 14817 MW; FEPF95657A2C81ACC CRC64;			
SQ SEQUENCE 122 AA.			
Query Match 100.0%; Score 139; DB 2; Length 122;			
Best Local Similarity 100.0%; Pred. No. 1.9e-13;			
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy 1 RILAVERTYLKDQQLGIGCGSGKLIK 26			
Db 19 RILAVERTYLKDQQLGIGCGSGKLIK 44			
RESULT 7			
Q7ZJR4	PRELIMINARY;	PRT; 122 AA.	
ID Q7ZJR4;			
AC Q7ZJR4;			
DT 01-JUN-2003 (TREMBLrel. 24, Created)			
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)			
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE Envelope glycoprotein (Fragment).			
GN Name=env;			
OS Human immunodeficiency virus 1.			
OC Viruses; Retroviridae; Lentivirus.			
OX NCBI_TaxID=11676;			
RN [1]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=22800244; PubMed=12921095; DOI=10.1089/088922203322231003;			
RA Swanson P.A., Devare S.G., Hackett J.R. Jr.; "Molecular Characterization of 39 HIV-1 Isolates Representing Group M (Subtypes A-G) and Group O: Sequence Analysis of gag p24, pol integrase, and env gp41."			
RT AIDS Res. Hum. Retroviruses 19:625-629(2003).			
RL DR EMBL; AY214095; AAO61815.1; -.			
DR HSSP; P12488; 1IM7.			
DR GO; GO:0016021; C:integral to membrane; IEA.			
DR GO; GO:0019028; C:viral capsid; IEA.			
DR GO; GO:0005198; F:structural molecule activity; IEA.			
DR InterPro; IPR000328; Env_GP41.			
DR PFam; PF00517; GP41; 1.			
KW Coat protein; Envelope protein; Glycoprotein; Transmembrane.			
FT NON-TER 1 1			
FT NON-TER 122 AA; 14763 MW; B9207B0EBBE4213AA CRC64;			
SQ SEQUENCE 122 AA.			
Query Match 100.0%; Score 139; DB 2; Length 122;			
Best Local Similarity 100.0%; Pred. No. 1.9e-13;			
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy 1 RILAVERTYLKDQQLGIGCGSGKLIK 26			
Db 19 RILAVERTYLKDQQLGIGCGSGKLIK 44			
RESULT 8			
Q9EA97	PRELIMINARY;	PRT; 122 AA.	
ID Q9EA97			
AC Q9EA97;			
DT 01-MAR-2001 (TREMBLrel. 16, Created)			
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)			
DE Envelope glycoprotein (Fragment).			
GN Name=env;			
OS Human immunodeficiency virus 1.			
OC Viruses; Retroviridae; Lentivirus.			
OX NCBI_TaxID=11676;			
RN [1]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=20134570; PubMed=10669328;			
RA Weidle P.J., Ganea C.E., Irwin K.L., Pieniazek D., McGowan J.P., Olivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A.;"Presence of human immunodeficiency virus (HIV) type 1, group M, non-B subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic diversity in the United States." J. Infect. Dis. 181:470-475(2000).			
RL DR EMBL; AF190955; AAG02317.1; -.			
DR HSSP; P12488; 1IM7.			
DR GO; GO:0016021; C:integral to membrane; IEA.			
DR GO; GO:0019028; C:viral capsid; IEA.			
DR GO; GO:0019031; C:viral envelope; IEA.			
DR GO; GO:0005198; F:structural molecule activity; IEA.			
DR InterPro; IPR000328; Env_GP41.			
DR PFam; PF00517; GP41; 1.			
KW Coat protein; Envelope protein; Glycoprotein; Transmembrane.			
FT NON-TER 1 1			
FT NON-TER 122 AA; 14763 MW; B9207B0EBBE4213AA CRC64;			
SQ SEQUENCE 122 AA.			
Query Match 100.0%; Score 139; DB 2; Length 122;			
Best Local Similarity 100.0%; Pred. No. 1.9e-13;			
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy 1 RILAVERTYLKDQQLGIGCGSGKLIK 26			
Db 19 RILAVERTYLKDQQLGIGCGSGKLIK 44			
RESULT 9			
Q9QIU3	PRELIMINARY;	PRT; 122 AA.	
ID Q9QIU3			
AC Q9QIU3;			
DT 01-MAY-2000 (TREMBLrel. 13, Created)			
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)			
DE Envelope glycoprotein (Fragment).			
GN Name=env;			
OS Human immunodeficiency virus 1.			
OC Viruses; Retroviridae; Lentivirus.			
OX NCBI_TaxID=11676;			
RN [1]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=21580799; PubMed=11724274;			
RA Caride E., Hertogs K., Larder B., Dehertog P., Brindeiro R., Machado E., de Sa C.A.M., Eyer-Silva W.A., Sion F.S., Passioni L.F.C.,			

RA Menezes J.A., Calazans A.R., Tanuri A.;  
 RT "Genotypic and phenotypic evidence of different drug-resistance  
 mutation patterns between B and non-B subtype isolates of human  
 immunodeficiency virus type 1 found in Brazilian patients failing  
 HAART.";  
 RT Virus Genes 23:193-202 (2001).

DR EMBL; AF165561; AAF08506.1; -.  
 DR HSSP; P12488; 1IM7.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0019028; C:viral capsid; IEA.  
 DR GO; GO:0019031; C:viral envelope; IEA.  
 DR GO; GO:0005198; F:structural molecule activity; IEA.  
 DR InterPro; IPR000328; Env\_GP41.  
 DR Pfam; PF00517; GP41; 1.  
 KW Coat protein; Envelope protein; Glycoprotein; Transmembrane.

FT NON-TER 1 122 AA; 122 MW; 14817 MW;

SQ SEQUENCE 122 AA; 14817 MW; 8D6099E5D3993205 CRC64;

Query Match 100.0%; Score 139; DB 2; Length 122;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-13;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RILAVERYLKDKDQQLLGIGWGCGSKLIC 26

Db 19 RILAVERYLKDKDQQLLGIGWGCGSKLIC 44

RESULT 10  
 ID Q9WQZ3 PRELIMINARY; PRT; 122 AA.

AC Q9WQZ3; PRELIMINARY; PRT; 122 AA.

AC

Db 17 RILAVERYLKDQQLGIWGCSGKLIK 42 FT NON-TER 144 144  
SQ SEQUENCE 144 AA; 16907 MW; A427C02C24218EEB CRC64;

RESULT 13 Query Match 100.0%; Score 139; DB 2; Length 144;  
ID Q698W3 PRELIMINARY; PRT; 134 AA.  
AC Q698W3; Best Local Similarity 100.0%; Pred. No. 2.3e-13;  
DT 25-OCT-2004 (TREMBLrel. 28, Created) Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN Name=env;  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroviridae; Lentiviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Ndembri N., Takehisa J., Zekeng L., Kobayashi E., Ngansop C.,  
RA Songok M.E., Takemura T., Ido E., Hayami M., Kaptue L., Ichimura H.;  
RT "Emergence of New Forms of HIV Type 1 in Cameroon, West-Central  
RT Africa.";  
RT Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.  
RL EMBL; AY541023; AAT07343.1; -.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR PFam; PF00517; GP41; 1.  
KW Coat protein; Envelope protein; Glycoprotein; Transmembrane.  
FT NON-TER 1 1  
FT NON-TER 134 134  
SQ SEQUENCE 134 AA; 16199 MW; A33CAA85195F8FDB CRC64;  
Query Match 100.0%; Score 139; DB 2; Length 134;  
Best Local Similarity 100.0%; Pred. No. 2.1e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLGIWGCSGKLIK 26  
Db 28 RILAVERYLKDQQLGIWGCSGKLIK 53

RESULT 14 Query Match 100.0%; Score 139; DB 2; Length 144;  
ID Q7ZCD6 PRELIMINARY; PRT; 144 AA.  
AC Q7ZCD6; Best Local Similarity 100.0%; Pred. No. 2.3e-13;  
DT 01-JUN-2003 (TREMBLrel. 24, Created) Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN Name=env;  
OS Human immunodeficiency virus 1.  
OC Viruses; Retroviridae; Lentiviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22679027; PubMed=12794544;  
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,  
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;  
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-  
RT 20) resistance in enfuvirtide-naive patients infected with subtype B  
RT and non-B HIV-1 strains.";  
RL Acquir. Immune Defic. Syndr. 33:134-139 (2003).  
DR EMBL; AY185383; AAO65658.1; -.  
DR HSSP; P04578; 1AIK.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Coat protein; Envelope protein; Glycoprotein; Transmembrane.  
FT NON-TER 1 1  
FT NON-TER 144 144  
SQ SEQUENCE 144 AA; 16887 MW; A139D1C53D318EEB CRC64;

RESULT 15 Query Match 100.0%; Score 139; DB 2; Length 144;  
ID Q7ZCD7 PRELIMINARY; PRT; 144 AA.  
AC Q7ZCD7; Best Local Similarity 100.0%; Pred. No. 2.3e-13;  
DT 01-JUN-2003 (TREMBLrel. 24, Created) Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN Name=env;  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovirovirus; Retroviridae; Lentiviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22679027; PubMed=12794544;  
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,  
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;  
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-  
RT 20) resistance in enfuvirtide-naive patients infected with subtype B  
RT and non-B HIV-1 strains.";  
RL Acquir. Immune Defic. Syndr. 33:134-139 (2003).  
DR EMBL; AY185384; AAO65659.1; -.  
DR HSSP; P04578; 1AIK.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Coat protein; Envelope protein; Glycoprotein; Transmembrane.  
FT NON-TER 1 1

Search completed: March 3, 2005, 17:22:15  
Job time : 178 secs

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OM protein - protein search, using sw model  
 Run on: March 3, 2005, 17:13:03 ; Search time 39 Seconds  
 (without alignments)  
 64.145 Million cell updates/sec

Title: US-09-733-239-1  
 Perfect score: 139  
 Sequence: 1 RILAVERYLKDQQQLIGIWGCGSKLIC 26  
 Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	139	100.0	357	2 S21996	envelope protein g
2	139	100.0	358	2 S21998	envelope protein g
3	139	100.0	853	2 S54384	envelope polyprotein
4	139	100.0	854	2 S13288	env protein - huma
5	139	100.0	855	1 VCLJZR	env polyprotein pr
6	139	100.0	856	1 VCLJH3	env polyprotein pr
7	139	100.0	856	1 VCLJV1	env polyprotein pr
8	139	100.0	861	1 VCLJLV	env polyprotein pr
9	138	99.3	357	2 S22004	envelope protein g
10	138	99.3	357	2 S21992	envelope protein g
11	138	99.3	357	2 S21994	envelope protein g
12	138	99.3	852	1 VCLJBR	env polyprotein -
13	138	99.3	856	1 A44963	env polyprotein pr
14	137	98.6	357	2 S21990	envelope protein g
15	135	97.1	358	2 S70417	envelope protein g
16	135	97.1	358	2 S22000	envelope protein g
17	135	97.1	358	2 S22002	envelope protein g
18	135	97.1	443	2 C41621	env polyprotein P
19	135	97.1	445	2 A41621	env polyprotein M
20	135	97.1	454	2 B41621	env polyprotein D
21	135	97.1	843	1 H44001	env polyprotein D
22	135	97.1	852	2 T12016	envelope glycoprot
23	135	97.1	855	1 VCLJA2	env polyprotein pr
24	135	97.1	856	1 VCLJ3W	env polyprotein pr
25	135	97.1	861	1 VCLJSC	env polyprotein pr
26	135	97.1	868	1 VCLJH4	env polyprotein -
27	134	96.4	859	1 VCLJMN	env polyprotein pr
28	134	96.4	729	1 VCLJKX	env polyprotein pr
29	132	95.0	861	1 VCLJKB	env polyprotein -
			847	2 T09448	env transmembrane
			847	2 S13289	env protein - huma
			846	1 VCLJND	env polyprotein pr
			854	1 VCLJSI	env protein - huma
			859	2 T01672	env protein -
			863	2 A53034	gag polyprotein -
			877	2 S49197	envelope protein p
			104	2 S52930	GP41 ENV protein -
			855	2 A45713	Env transmembrane
			861	2 A47665	env polyprotein pr
			881	2 S30368	env protein - huma
			151	2 S30453	env protein - huma
			151	2 S30451	env protein - huma

#### ALIGNMENTS

RESULT 1  
 S21996  
 envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 27L)  
 C;Species: human immunodeficiency virus type 1, HIV-1  
 C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
 C;Accession: S70422; S21996  
 R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
 A;Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by sequence comparison of gp120/gp41  
 A;Reference number: S70417; MUID:92144209; PMID:1736940  
 A;Accession: S70422  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-357 <ST2>  
 A;Cross-references: UNIPROT:Q78119; EMBL:X61356; NID:960181; PIDN:CAA43624.1; PID:910671;  
 A;Experimental source: patient 27L  
 A;Note: submitted to the EMBL Data Library, July 1991  
 C;Superfamily: type B retrovirus env polyprotein

Query Match 100.0%; Score 139; DB 2; Length 357;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-13; Mismatches 0; Indels 0; Gaps 0;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY	1 RILAVERYLKDQQLLGIGCWSGKGLIC 26
Db	80 RILAVERYLKDQQLLGIGCWSGKGLIC 105

RESULT 2  
 S21998  
 envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 28)  
 C;Species: human immunodeficiency virus type 1, HIV-1  
 C;Variety: isolate 28  
 C;Accession: S21998; S70425  
 R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
 Submitted to the EMBL Data Library, July 1991  
 A;Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined by sequence comparison of gp120/gp41  
 A;Reference number: S70417; MUID:92144209; PMID:1736940  
 A;Accession: S21998  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-358 <ST2>  
 A;Cross-references: UNIPROT:Q78120; EMBL:X61359; NID:960182; PIDN:CAA43630.1; PID:960183  
 R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
 A;Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by sequence comparison of gp120/gp41  
 A;Reference number: S70417; MUID:92144209; PMID:1736940  
 A;Accession: S70425  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-222 'X' 224-358 <ST2>  
 A;Cross-references: EMBL:X61359; NID:960182; PIDN:CAA43630.1; PID:960183

C;Superfamily: type E retrovirus env polyprotein

Query Match	100.0%	Score 139;	DB 2;	Length 358;
Best Local Similarity	100.0%	Pred. No. 2.2e-13;		
Matches 26;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy 1 RILAVERYLKDQQLGIWGCGSKLIC 26  
Db 81 RILAVERYLKDQQLGIWGCGSKLIC 106

**RESULT 3**  
S54384 envelope polyprotein - human immunodeficiency virus type 1  
C;Species: human immunodeficiency virus type 1, HIV-1  
C;Accession: S54384  
R/Theodore, T.; Buckler-White, A.J.  
Submitted to the EMBL Data Library, July 1989  
A;Reference number: S54384  
A;Accession: S54384  
A;Molecule type: genomic RNA  
A;Residues: 1-853 <THE>  
A;Cross-references: UNIPROT:P12487; EMBL:M22639; NID:g329377; PID:g329373  
C;Superfamily: type E retrovirus env polyprotein  
C;Keywords: polyprotein

Query Match 100.0% Score 139; DB 2; Length 853;  
Best Local Similarity 100.0% Pred. No. 5.4e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLGIWGCGSKLIC 26  
Db 576 RILAVERYLKDQQLGIWGCGSKLIC 601

**RESULT 4**  
S13288 env protein - human immunodeficiency virus type 1, HIV-1  
C;Species: human immunodeficiency virus type 1, HIV-1  
C;Accession: S13288  
R/O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A.  
Nature 348, 69-73, 1990  
A;Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120  
A;Reference number: S13288; MUID:91043044; PMID:2172833  
A;Accession: S13288  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-854 <OBR>  
A;Cross-references: UNIPROT:Q85582; UNIPROT:Q72502; UNIPROT:Q90178; UNIPROT:Q78243; UNIPROT:Q03973  
C;Superfamily: type E retrovirus env polyprotein

Query Match 100.0% Score 139; DB 2; Length 854;  
Best Local Similarity 100.0% Pred. No. 5.4e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLGIWGCGSKLIC 26  
Db 577 RILAVERYLKDQQLGIWGCGSKLIC 602

**RESULT 5**  
VCLJZR env polyprotein precursor - human immunodeficiency virus Zr-6  
N;Alternate names: coat polyprotein  
C;Species: human immunodeficiency virus Zr-6  
C;Accession: D26192  
C;Date: 30-Sep-1987 #sequence\_revision 30-Sep-1987 #text\_change 09-Jul-2004  
R/Srinivasan, A.; Anand, R.; York, D.; Ranganathan, P.; Schochetman, G.; Cu  
Gene 52, 71-82, 1987  
A;Title: Molecular characterization of human immunodeficiency virus from Zaire: nucleotid  
A;Reference number: A93355; MUID:85111157; PMID:2982104  
A;Accession: A03974

A;Reference number: A26192; MUID:87248097; PMID:3036660  
A;Accession: D26192  
A;Molecule type: DNA  
A;Residues: 1-855 <SR>  
A;Cross-references: UNIPROT:P04580; GB:K03458; GB:MI6322; NID:g329398; PIDN:AAA45380.1; I  
C;Genetics:  
A;Gene: env  
C;Superfamily: type E retrovirus env polyprotein  
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein  
F;1-19/Domain: signal sequence #status predicted <SIG>  
F;20-855/Product: env polyprotein #status predicted <MAT>  
F;501-855/Product: exterior membrane glycoprotein #status predicted <TMM>  
F;87,129,140,145,154,158,186,189,199,236,243,264,278,291,297,333,340,355,386,392,398,404,  
Query Match 100.0%; Score 139; DB 1; Length 855;  
Best Local Similarity 100.0%; pred. No. 5.4e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 RILAVERYLKDQQLGIWGCGSKLIC 26  
Db 578 RILAVERYLKDQQLGIWGCGSKLIC 603

**RESULT 6**  
VCLJH3 env polyprotein precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)  
N;Alternate names: coat polyprotein  
C;Species: human immunodeficiency virus type 1, HIV-1  
A;Note: host Homo sapiens (man)  
C;Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 09-Jul-2004  
C;Accession: A03973  
R/Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Dorar  
Nberger, J.A.; Papas, T.S.; Ghrayeb, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.  
Nature 313, 277-284, 1985  
A;Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.  
A;Reference number: A93353; MUID:85111123; PMID:2578615  
A;Accession: A03973  
A;Molecule type: DNA  
A;Residues: 1-856 <RAT>  
A;Cross-references: UNIPROT:P03375; GB:MI5654; GB:K02008; GB:K02010; NID:9326;  
C;Genetics:  
A;Gene: env  
C;Superfamily: type E retrovirus env polyprotein  
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein  
F;1-30/Domain: signal sequence #status predicted <SIG>  
F;31-511/Product: exterior membrane glycoprotein #status predicted <EXT>  
F;512-856/Product: transmembrane glycoprotein #status predicted <TMM>  
F;88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406,  
F;611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predict  
Query Match 100.0%; Score 139; DB 1; Length 856;  
Best Local Similarity 100.0%; pred. No. 5.4e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 RILAVERYLKDQQLGIWGCGSKLIC 26  
Db 579 RILAVERYLKDQQLGIWGCGSKLIC 604

**RESULT 7**  
VCLJVL env polyprotein precursor - human immunodeficiency virus type 1 (isolate IV)  
N;Alternate names: coat polyprotein  
C;Species: human immunodeficiency virus type 1, HIV-1  
A;Note: host Homo sapiens (man)  
C;Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 09-Jul-2004  
C;Accession: A03974  
R/Muesing, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon, D.J.  
Nature 313, 450-458, 1985  
A;Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retrovi  
A;Reference number: A93355; MUID:85111157; PMID:2982104  
A;Accession: A03974

A;Molecule type: DNA  
A;Residues: 1-856 <MUE>  
A;Cross-references: UNIPROT:P03376; GB:K02083; NID:9555008; PIDN:AAB59873.1; PMID:9328559  
C;Genetics:  
A;Gene: env  
C;Superfamily: type E retrovirus env polyprotein  
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein  
F:1-30/Domain: signal sequence #status predicted <SIG>  
F:31-511/Product: exterior membrane glycoprotein #status predicted <EXT>  
F:512-856/Product: transmembrane glycoprotein #status predicted <TM>  
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406  
F:611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match 100.0%; Score 139; DB 1; Length 856;  
Best Local Similarity 100.0%; Pred. No. 5.4e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 RILAVERYLKDKQQLGIWGCGSKLIC 26  
Db 579 RILAVERYLKDKQQLGIWGCGSKLIC 604

RESULT 8  
VCLJLV  
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LAV-1a)  
N:Alternate names: coat polyprotein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A;Note: host Homo sapiens (man)  
C;Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 09-Jul-2004  
C;Accession: A03975  
R;Wain-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M.  
Cell 40, 9-17, 1985  
A;Title: Nucleotide sequence of the AIDS virus, LAV.  
A;Reference number: A90866; MUID:85099333; PMID:2981635  
A;Accession: A03975  
A;Molecule type: DNA  
A;Residues: 1-861 <WAII>  
A;Cross-references: UNIPROT:P03377; GB:K02013; NID:9326417; PIDN:AAB59751.1; PMID:9326424  
C;Genetics:  
A;Gene: env  
C;Superfamily: type E retrovirus env polyprotein  
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein  
F:1-30/Domain: signal sequence #status predicted <SIG>  
F:31-516/Product: exterior membrane glycoprotein #status predicted <EXT>  
F:517-861/Product: transmembrane glycoprotein #status predicted <TM>  
F:88,136,141,146,161,165,191,202,239,246,267,281,294,300,306,337,344,361,391,397,402,411  
F:616,621,630,642,679,755,821/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 139; DB 1; Length 861;  
Best Local Similarity 100.0%; Pred. No. 5.5e-13;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 RILAVERYLKDKQQLGIWGCGSKLIC 26  
Db 584 RILAVERYLKDKQQLGIWGCGSKLIC 609

RESULT 9  
S22004  
env envelope protein gp120/gp41 - human immunodeficiency virus type 1, HIV-1  
C;Species: human immunodeficiency virus type 1, HIV-1  
A;Variety: isolate 4B  
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C;Accession: S22004; S70419  
R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
submitted to the EMBL Data Library, July 1991  
A;Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined  
A;Reference number: S21990  
A;Accession: S22004  
A;Molecule type: DNA  
A;Residues: 1-357 <STB1>  
A;Cross-references: UNIPROT:Q78155; EMBL:X61353; NID:g60188; PIDN:CAA43618.1; PMID:960189  
R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
A;Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebr  
A;Reference number: S70417; MUID:92144209; PMID:1736940  
A;Accession: S70419  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-292,'X',294-357 <STE2>  
A;Cross-references: EMBL:X61353; NID:g60188  
C;Superfamily: type E retrovirus env polyprotein  
Query Match 99.3%; Score 138; DB 2; Length 357;  
Best Local Similarity 96.2%; Pred. No. 3.1e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 RILAVERYLKDKQQLGIWGCGSKLIC 26  
Db 80 RILAVERYLKDKQQLGIWGCGSKLIC 105

RESULT 10  
S22006  
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 4L)  
C;Species: human immunodeficiency virus type 1, HIV-1  
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C;Accession: S70420; S22006  
R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
A;Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebr  
A;Reference number: S70417; MUID:92144209; PMID:1736940  
A;Accession: S70420  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-357 <ST2>  
A;Cross-references: UNIPROT:Q78156; EMBL:X61354; NID:g60190; PIDN:CAA43620.1; PMID:960191  
A;Experimental source: patient L  
A;Note: submitted to the EMBL Data Library, July 1991  
C;Superfamily: type E retrovirus env polyprotein  
Query Match 99.3%; Score 138; DB 2; Length 357;  
Best Local Similarity 96.2%; Pred. No. 3.1e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 RILAVERYLKDKQQLGIWGCGSKLIC 26  
Db 80 RILAVERYLKDKQQLGIWGCGSKLIC 105

RESULT 11  
S21992  
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 22)  
C;Species: human immunodeficiency virus type 1, HIV-1  
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C;Accession: S70424; S21992  
R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
A;Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebr  
A;Reference number: S70417; MUID:92144209; PMID:1736940  
A;Accession: S70424  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-357 <ST2>  
A;Cross-references: UNIPROT:Q78112; EMBL:X61358; NID:g60177; PIDN:CAA43628.1; PMID:960178  
A;Experimental source: patient 22  
A;Note: submitted to the EMBL Data Library, July 1991  
C;Superfamily: type E retrovirus env polyprotein  
Query Match 99.3%; Score 138; DB 2; Length 357;  
Best Local Similarity 96.2%; Pred. No. 3.1e-13;  
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 RILAVERYLKDKQQLGIWGCGSKLIC 26  
Db 80 RILAVERYLKDKQQLGIWGCGSKLIC 105

RESULT 12  
S21994 envelope protein gp120/gp41 - human immunodeficiency virus type 1, HIV-1

C;Species: human immunodeficiency virus type 1, HIV-1  
 A;Variety: isolate 27B  
 C;Accession: S21994 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
 R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
 submitted to the EMBL Data Library, July 1991  
 A;Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined  
 A;Reference number: S21990  
 A;Accession: S21994  
 A;Molecule type: DNA  
 A;Residues: 1-357 <STE1>  
 A;Cross-references: UNIPROT:Q78118; EMBL:X61355; NID:960179; PIDN:CAA43622.1; PID:g60180  
 R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
 A;Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebr  
 A;Reference number: S70417; MUID:92144209; PMID:1736940  
 A;Accession: S70421  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-140, 'X', 142-312, 'X', 314-357 <STE2>  
 A;Cross-references: EMBL:X61355; NID:960179  
 C;Superfamily: type E retrovirus env polyprotein

Query Match 99.3%; Score 138; DB 2; Length 357;  
 Best Local Similarity 96.2%; Pred. No. 3.1e-13;  
 Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 RILAVERYLKDQQLGIWGCGSKLIC 26  
 Db 80 RVLAVERYLKDQQLGIWGCGSKLIC 105  
 RESULT 15  
 S21990 envelope protein gp120/gp41 - human immunodeficiency virus type 1  
 C;Species: human immunodeficiency virus type 1, HIV-1  
 A;Variety: isolate 20  
 C;Accession: S21990; S70423  
 R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
 Submitted to the EMBL Data Library, July 1991  
 A;Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined  
 A;Reference number: S21990  
 A;Molecule type: DNA  
 A;Residues: 1-357 <STE1>  
 A;Cross-references: UNIPROT:Q78100; EMBL:X61357; NID:960175; PIDN:CAA43626.1; PID:g60176  
 R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
 A;Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebr  
 A;Reference number: S70417; MUID:92144209; PMID:1736940  
 A;Accession: S70423  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-332, 'X', 334-357 <STE2>  
 A;Cross-references: EMBL:X61357; NID:960175; PIDN:CAA43626.1; PID:g60176  
 C;Superfamily: type E retrovirus env polyprotein

Query Match 97.1%; Score 135; DB 2; Length 357;  
 Best Local Similarity 92.3%; Pred. No. 9e-13;  
 Matches 24; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 RILAVERYLKDQQLGIWGCGSKLIC 26  
 Db 80 RVLAVERYLKDQQLGIWGCGSKLIC 105  
 Search completed: March 3, 2005, 17:22:58  
 Job time : 39 secs

RESULT 14  
 A44963 env polyprotein precursor - human immunodeficiency virus type 1 (isolate Z321)  
 N;Alternate names: coat polyprotein  
 N;Contains: coat protein gp120; coat protein gp41; coat protein gp120 #status predicted <CP1>  
 F;517-852/Product: coat protein gp41 #status predicted <CP2>  
 A;Accession: A31667  
 A;Molecule type: DNA  
 A;Residues: 1-852 <ANA>  
 A;Cross-references: UNIPROT:P12488  
 C;Superfamily: type E retrovirus env polyprotein  
 C;Keywords: capsid protein; coat protein; polyprotein; transmembrane protein  
 F;1-516/Product: coat protein gp120 #status predicted <CP1>  
 F;517-852/Product: coat protein gp41 #status predicted <CP2>  
 Query Match 99.3%; Score 138; DB 1; Length 852;  
 Best Local Similarity 96.2%; Pred. No. 7.7e-13;  
 Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 RILAVERYLKDQQLGIWGCGSKLIC 26  
 Db 575 RVLAVERYLKDQQLGIWGCGSKLIC 600

RESULT 15  
 A44963 env polyprotein precursor - human immunodeficiency virus type 1 (isolate Z321)  
 N;Contains: coat polyprotein  
 N;Contains: coat protein gp120; coat protein gp41